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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/581,241

DATE: 11/13/2001
 TIME: 13:41:33

Input Set : A:\193582USOPCT.ST25.txt
 Output Set: N:\CRF3\11132001\I581241.raw

3 <110> APPLICANT: HATTORI, NORIAKI
 4 MURAKAMI, SEIJI
 6 <120> TITLE OF INVENTION: LUCIFERASE AND A METHOD FOR DETECTING INTRACELLULAR ATP
 USING THE SAME

8 <130> FILE REFERENCE: 193582US-3524-7126-0 PCT

10 <140> CURRENT APPLICATION NUMBER: 09/581241

11 <141> CURRENT FILING DATE: 2000-06-26

13 <150> PRIOR APPLICATION NUMBER: JP97/361022

14 <151> PRIOR FILING DATE: 1997-12-26

16 <160> NUMBER OF SEQ ID NOS: 6

18 <170> SOFTWARE: PatentIn version 3.1

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 23

22 <212> TYPE: DNA

23 <213> ORGANISM: ARTIFICIAL SEQUENCE

25 <220> FEATURE:

26 <223> OTHER INFORMATION: SYNTHETIC DNA

28 <400> SEQUENCE: 1

29 tgttggtactt aagaaaggaa aat

32 <210> SEQ ID NO: 2

33 <211> LENGTH: 23

34 <212> TYPE: DNA

35 <213> ORGANISM: ARTIFICIAL SEQUENCE

37 <220> FEATURE:

38 <223> OTHER INFORMATION: SYNTHETIC DNA

40 <400> SEQUENCE: 2

41 acagctcccg gaagctcacc agc

44 <210> SEQ ID NO: 3

45 <211> LENGTH: 1644

46 <212> TYPE: DNA

47 <213> ORGANISM: Luciola lateralis

49 <220> FEATURE:

50 <221> NAME/KEY: CDS

51 <222> LOCATION: (1)..(1644)

52 <223> OTHER INFORMATION:

55 <400> SEQUENCE: 3

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57 Met Glu Asn Met Glu Asn Asp Glu Asn Ile Val Tyr Gly Pro Glu Pro

58 1 5 10 15

60 ttt tac cct att gaa gag gga tct gct gga gca caa ttg cgc aag tat

61 Phe Tyr Pro Ile Glu Glu Gly Ser Ala Gly Ala Gln Leu Arg Lys Tyr

62 20 25 30

64 atg gat cga tat gca aaa ctt gga gca att gct ttt act aac gca ctt

65 Met Asp Arg Tyr Ala Lys Leu Gly Ala Ile Ala Phe Thr Asn Ala Leu

66 35 40 45

68 acc ggt gtc gat tat acg tac gcc gaa tac tta gaa aaa tca tgc tgt

69 Thr Gly Val Asp Tyr Thr Tyr Ala Glu Tyr Leu Glu Lys Ser Cys Cys

70 50 55 60

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72	cta gga gag gct tta aag aat tat ggt ttg gtt gtt gat gga aga att	240
73	Leu Gly Glu Ala Leu Lys Asn Tyr Gly Leu Val Val Asp Gly Arg Ile	
74	65 70 75 80	
76	gcg tta tgc agt gaa aac tgt gaa gaa ttc ttt att cct gta tta gcc	288
77	Ala Leu Cys Ser Glu Asn Cys Glu Glu Phe Phe Ile Pro Val Leu Ala	
78	85 90 95	
80	ggt tta ttt ata ggt gtc ggt gtg gct cca act aat gag att tac act	336
81	Gly Leu Phe Ile Gly Val Gly Val Ala Pro Thr Asn Glu Ile Tyr Thr	
82	100 105 110	
84	cta cgt gaa ttg gtt cac agt tta ggc atc tct aag cca aca att gta	384
85	Leu Arg Glu Leu Val His Ser Leu Gly Ile Ser Lys Pro Thr Ile Val	
86	115 120 125	
88	ttt agt tct aaa aaa gga tta gat aaa gtt ata act gta caa aaa acg	432
89	Phe Ser Ser Lys Lys Gly Leu Asp Lys Val Ile Thr Val Gln Lys Thr	
90	130 135 140	
92	gta act gct att aaa acc att gtt ata ttg gac agc aaa gtg gat tat	480
93	Val Thr Ala Ile Lys Thr Ile Val Ile Leu Asp Ser Lys Val Asp Tyr	
94	145 150 155 160	
96	aga ggt tat caa tcc atg gac aac ttt att aaa aaa aac act cca caa	528
97	Arg Gly Tyr Gln Ser Met Asp Asn Phe Ile Lys Lys Asn Thr Pro Gln	
98	165 170 175	
100	ggt ttc aaa gga tca agt ttt aaa act gta gaa gtt aac cgc aaa gaa	576
101	Gly Phe Lys Gly Ser Ser Phe Lys Thr Val Glu Val Asn Arg Lys Glu	
102	180 185 190	
104	caa gtt gct ctt ata atg aac tct tgc ggt tca acc ggt ttg cca aaa	624
105	Gln Val Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys	
106	195 200 205	
108	ggt gtg caa ctt act cat gaa aat ttg gtc act aga ttt tct cac gct	672
109	Gly Val Gln Leu Thr His Glu Asn Leu Val Thr Arg Phe Ser His Ala	
110	210 215 220	
112	aga gat cca att tat gga aac caa gtt tca cca ggc acg gct att tta	720
113	Arg Asp Pro Ile Tyr Gly Asn Gln Val Ser Pro Gly Thr Ala Ile Leu	
114	225 230 235 240	
116	act gta gta cca ttc cat cat ggt ttt ggt atg ttt act act tta ggc	768
117	Thr Val Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly	
118	245 250 255	
120	tat cta act tgt ggt ttt cgt att gtc atg tta acg aaa ttt gac gaa	816
121	Tyr Leu Thr Cys Gly Phe Arg Ile Val Met Leu Thr Lys Phe Asp Glu	
122	260 265 270	
124	gag act ttt tta aaa aca ctg caa gat tac aaa tgt tca agc gtt att	864
125	Glu Thr Phe Leu Lys Thr Leu Gln Asp Tyr Lys Cys Ser Ser Val Ile	
126	275 280 285	
128	ctt gta ccg act ttg ttt gca att ctt aat aga agt gaa tta ctc gat	912
129	Leu Val Pro Thr Leu Phe Ala Ile Leu Asn Arg Ser Glu Leu Leu Asp	
130	290 295 300	
132	aaa tat gat tta tca aat tta gtt gaa att gca tct ggc gga gca cct	960
133	Lys Tyr Asp Leu Ser Asn Leu Val Glu Ile Ala Ser Gly Gly Ala Pro	
134	305 310 315 320	
136	tta tct aaa gaa att ggt gaa gct gtt gct aga cgt ttt aat tta ccg	1008

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137 Leu Ser Lys Glu Ile Gly Glu Ala Val Ala Arg Arg Phe Asn Leu Pro
138                               325                               330                               335
140 ggt gtt cgt caa ggc tat ggt tta aca gaa aca acc tct gca att att      1056
141 Gly Val Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Ile
142                               340                               345                               350
144 atc aca ccg gaa ggc gat gat aaa cca ggt gct tct ggc aaa gtt gtg      1104
145 Ile Thr Pro Glu Gly Asp Asp Lys Pro Gly Ala Ser Gly Lys Val Val
146                               355                               360                               365
148 cca tta ttt aaa gca aaa gtt atc gat ctt gat act aaa aaa act ttg      1152
149 Pro Leu Phe Lys Ala Lys Val Ile Asp Leu Asp Thr Lys Lys Thr Leu
150                               370                               375                               380
152 ggc ccg aac aga cgt gga gaa gtt tgt gta aag ggt cct atg ctt atg      1200
153 Gly Pro Asn Arg Arg Gly Glu Val Cys Val Lys Gly Pro Met Leu Met
154 385                               390                               395                               400
156 aaa ggt tat gta gat aat cca gaa gca aca aga gaa atc ata gat gaa      1248
157 Lys Gly Tyr Val Asp Asn Pro Glu Ala Thr Arg Glu Ile Ile Asp Glu
158                               405                               410                               415
160 gaa ggt tgg ttg cac aca gga gat att ggg tat tac gat gaa gaa aaa      1296
161 Glu Gly Trp Leu His Thr Gly Asp Ile Gly Tyr Tyr Asp Glu Glu Lys
162                               420                               425                               430
164 cat ttc ttt atc gtg gat cgt ttg aag tct tta atc aaa tac aaa gga      1344
165 His Phe Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly
166                               435                               440                               445
168 tat caa gta cca cct gct gaa tta gaa tct gtt ctt ttg caa cat cca      1392
169 Tyr Gln Val Pro Pro Ala Glu Leu Glu Ser Val Leu Leu Gln His Pro
170                               450                               455                               460
172 aat att ttt gat gcc ggc gtt gct ggc gtt cca gat cct ata gct ggt      1440
173 Asn Ile Phe Asp Ala Gly Val Ala Gly Val Pro Asp Pro Ile Ala Gly
174 465                               470                               475                               480
176 gag ctt ccg gga gct gtt gtt gta ctt aag aaa gga aaa tct atg act      1488
177 Glu Leu Pro Gly Ala Val Val Val Leu Lys Lys Gly Lys Ser Met Thr
178                               485                               490                               495
180 gaa aaa gaa gta atg gat tac gtt gct agt caa gtt tca aat gca aaa      1536
181 Glu Lys Glu Val Met Asp Tyr Val Ala Ser Gln Val Ser Asn Ala Lys
182                               500                               505                               510
184 cgt ttg cgt ggt ggt gtc cgt ttt gtg gac gaa gta cct aaa ggt ctc      1584
185 Arg Leu Arg Gly Gly Val Arg Phe Val Asp Glu Val Pro Lys Gly Leu
186                               515                               520                               525
188 act ggt aaa att gac ggt aaa gca att aga gaa ata ctg aag aaa cca      1632
189 Thr Gly Lys Ile Asp Gly Lys Ala Ile Arg Glu Ile Leu Lys Lys Pro
190                               530                               535                               540
192 gtt gct aag atg
193 Val Ala Lys Met
194 545
197 <210> SEQ ID NO: 4
198 <211> LENGTH: 548
199 <212> TYPE: PRT
200 <213> ORGANISM: Luciola lateralis
202 <400> SEQUENCE: 4

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204 Met Glu Asn Met Glu Asn Asp Glu Asn Ile Val Tyr Gly Pro Glu Pro
205 1 5 10 15
208 Phe Tyr Pro Ile Glu Glu Gly Ser Ala Gly Ala Gln Leu Arg Lys Tyr
209 20 25 30
212 Met Asp Arg Tyr Ala Lys Leu Gly Ala Ile Ala Phe Thr Asn Ala Leu
213 35 40 45
216 Thr Gly Val Asp Tyr Thr Tyr Ala Glu Tyr Leu Glu Lys Ser Cys Cys
217 50 55 60
220 Leu Gly Glu Ala Leu Lys Asn Tyr Gly Leu Val Val Asp Gly Arg Ile
221 65 70 75 80
224 Ala Leu Cys Ser Glu Asn Cys Glu Glu Phe Phe Ile Pro Val Leu Ala
225 85 90 95
228 Gly Leu Phe Ile Gly Val Gly Val Ala Pro Thr Asn Glu Ile Tyr Thr
229 100 105 110
232 Leu Arg Glu Leu Val His Ser Leu Gly Ile Ser Lys Pro Thr Ile Val
233 115 120 125
236 Phe Ser Ser Lys Lys Gly Leu Asp Lys Val Ile Thr Val Gln Lys Thr
237 130 135 140
240 Val Thr Ala Ile Lys Thr Ile Val Ile Leu Asp Ser Lys Val Asp Tyr
241 145 150 155 160
244 Arg Gly Tyr Gln Ser Met Asp Asn Phe Ile Lys Lys Asn Thr Pro Gln
245 165 170 175
248 Gly Phe Lys Gly Ser Ser Phe Lys Thr Val Glu Val Asn Arg Lys Glu
249 180 185 190
252 Gln Val Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys
253 195 200 205
256 Gly Val Gln Leu Thr His Glu Asn Leu Val Thr Arg Phe Ser His Ala
257 210 215 220
260 Arg Asp Pro Ile Tyr Gly Asn Gln Val Ser Pro Gly Thr Ala Ile Leu
261 225 230 235 240
264 Thr Val Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly
265 245 250 255
268 Tyr Leu Thr Cys Gly Phe Arg Ile Val Met Leu Thr Lys Phe Asp Glu
269 260 265 270
272 Glu Thr Phe Leu Lys Thr Leu Gln Asp Tyr Lys Cys Ser Ser Val Ile
273 275 280 285
276 Leu Val Pro Thr Leu Phe Ala Ile Leu Asn Arg Ser Glu Leu Leu Asp
277 290 295 300
280 Lys Tyr Asp Leu Ser Asn Leu Val Glu Ile Ala Ser Gly Gly Ala Pro
281 305 310 315 320
284 Leu Ser Lys Glu Ile Gly Glu Ala Val Ala Arg Arg Phe Asn Leu Pro
285 325 330 335
288 Gly Val Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Ile
289 340 345 350
292 Ile Thr Pro Glu Gly Asp Asp Lys Pro Gly Ala Ser Gly Lys Val Val
293 355 360 365
296 Pro Leu Phe Lys Ala Lys Val Ile Asp Leu Asp Thr Lys Lys Thr Leu
297 370 375 380
300 Gly Pro Asn Arg Arg Gly Glu Val Cys Val Lys Gly Pro Met Leu Met

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301 385          390          395          400
304 Lys Gly Tyr Val Asp Asn Pro Glu Ala Thr Arg Glu Ile Ile Asp Glu
305          405          410          415
308 Glu Gly Trp Leu His Thr Gly Asp Ile Gly Tyr Tyr Asp Glu Glu Lys
309          420          425          430
312 His Phe Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly
313          435          440          445
316 Tyr Gln Val Pro Pro Ala Glu Leu Glu Ser Val Leu Leu Gln His Pro
317          450          455          460
320 Asn Ile Phe Asp Ala Gly Val Ala Gly Val Pro Asp Pro Ile Ala Gly
321 465          470          475          480
324 Glu Leu Pro Gly Ala Val Val Val Leu Lys Lys Gly Lys Ser Met Thr
325          485          490          495
328 Glu Lys Glu Val Met Asp Tyr Val Ala Ser Gln Val Ser Asn Ala Lys
329          500          505          510
332 Arg Leu Arg Gly Gly Val Arg Phe Val Asp Glu Val Pro Lys Gly Leu
333          515          520          525
336 Thr Gly Lys Ile Asp Gly Lys Ala Ile Arg Glu Ile Leu Lys Lys Pro
337          530          535          540
340 Val Ala Lys Met
341 545
344 <210> SEQ ID NO: 5
345 <211> LENGTH: 1644
346 <212> TYPE: DNA
347 <213> ORGANISM: Luciola lateralis
349 <220> FEATURE:
350 <221> NAME/KEY: CDS
351 <222> LOCATION: (1)..(1644)
352 <223> OTHER INFORMATION:
355 <400> SEQUENCE: 5
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358 1          5          10          15
360 ttt tac cct att gaa gag gga tct gct gga gca caa ttg cgc aag tat      96
361 Phe Tyr Pro Ile Glu Glu Gly Ser Ala Gly Ala Gln Leu Arg Lys Tyr
362          20          25          30
364 atg gat cga tat gca aaa ctt gga gca att gct ttt act aac gca ctt      144
365 Met Asp Arg Tyr Ala Lys Leu Gly Ala Ile Ala Phe Thr Asn Ala Leu
366          35          40          45
368 acc ggt gtc gat tat acg tac gcc gaa tac tta gaa aaa tca tgc tgt      192
369 Thr Gly Val Asp Tyr Thr Tyr Ala Glu Tyr Leu Glu Lys Ser Cys Cys
370          50          55          60
372 cta gga gag gct tta aag aat tat ggt ttg gtt gtt gat gga aga att      240
373 Leu Gly Glu Ala Leu Lys Asn Tyr Gly Leu Val Val Asp Gly Arg Ile
374 65          70          75          80
376 gcg tta tgc agt gaa aac tgt gaa gaa ttc ttt att cct gta tta gcc      288
377 Ala Leu Cys Ser Glu Asn Cys Glu Glu Phe Phe Ile Pro Val Leu Ala
378          85          90          95
380 ggt tta ttt ata ggt gtc ggt gtg gct cca act aat gag att tac act      336

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VERIFICATION SUMMARY

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